WHAT IS CLAIMED IS:

1	1. A method for identifying a compound that modulates cell cycle		
2	arrest, the method comprising the steps of:		
3	(i) contacting a cell comprising a target polypeptide or fragment thereof or		
4	inactive variant thereof, selected from the group consisting of flap structure specific		
5	endonuclease 1 (FEN1), protein kinase C ζ (PKC- ζ), phospholipase C- β 1 (PLC- β 1),		
6	protein tyrosine kinase 2 (FAK), protein tyrosine kinase 2b (FAK2), casein kinase 2		
7	(CK2), cMET tyrosine kinase (cMET), REV1 dCMP transferase (REV1),		
8	apurinic/apyrimidinic nuclease 1 (APE1), cyclin dependent kinase 3 (CDK3), PIM1		
9	kinase (PIM1), cell division cycle 7 kinase (CDC7L1), cyclin dependent kinase 7		
10	(CDK7), cytokine inducible kinase (CNK), potentially prenylated protein tyrosine		
11	phosphatase (PRL-3), serine threonine kinase 2 (STK2) or (NEK4), cyclin dependent		
12	serine threonine kinase (NKIAMRE), or histone acetylase (HBO1), or fragment thereof		
13	with the compound, the target polypeptide encoded by the complement of a nucleic acid		
14	that hybridizes under stringent conditions to a nucleic acid encoding a polypeptide having		
15	an amino acid sequence selected from the group consisting of SEQ ID NO:14, 2, 4, 6, 8,		
16	10, 12, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, and 36; and		
17	(ii) determining the chemical or phenotypic effect of the compound upon		
18	the cell comprising the target polypeptide or fragment thereof or inactive variant thereof,		
19	thereby identifying a compound that modulates cell cycle arrest.		
1	2. The method of claim 1, wherein the chemical or phenotypic effect		
2	is determined by measuring enzymatic activity selected from the group consisting of		
3	nuclease activity, kinase activity, lipase activity, transferase activity, phosphatase activity		
4	and acetylase activity.		
1	3. The method of claim 1, wherein the chemical or phenotypic effect		
2	is determined by measuring cellular proliferation.		
1	4. The method of claim 3, wherein the cellular proliferation is		
2	measured by assaying fluorescent marker level or DNA synthesis.		
1	5. The method of claim 4, wherein DNA synthesis is measured by ³ H		
2	thymidine incorporation, BrdU incorporation, or Hoescht staining.		

The method of claim 4, wherein the fluorescent marker is selected 1 6. from the group consisting of a cell tracker dye or green fluorescent protein. 2 The method of claim 1, wherein modulation is activation of cell 7. 1 2 cycle arrest. The method of claim 1, wherein modulation is activation of cancer 1 8. 2 cell cycle arrest. The method of claim 1, wherein the host cell is a cancer cell. 9. 1 The method of claim 9, wherein the cancer cell is a breast, prostate, 1 10. 2 colon, or lung cancer cell. The method of claim 9, wherein the cancer cell is a transformed 11. 1 2 cell line. The method of claim 11, wherein the transformed cell line is A549, 1 12. 2 PC3, H1299, MDA-MB-231, MCF7, or HeLa. The method of claim 9, wherein the cancer cell is p53 null or 13. 1 2 mutant. The method of claim 9, wherein the cancer cell is p53 wild-type. 14. 1 The method of claim 1, wherein the polypeptide is recombinant. 1 15. The method of claim 1, wherein the polypeptide is encoded by a 16. 1 nucleic acid comprising a sequence of SEQ ID NO:13, 1, 3, 5, 7, 9, 11, 15, 17, 19, 21, 23, 2 3 25, 27, 29, 31, 33, or 35. The method of claim 1, wherein the compound is an antibody. 17. 1 The method of claim 1, wherein the compound is a small organic 1 18. 2 molecule. The method of claim 1, wherein the compound is an antisense 1 19.

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molecule.

1	20).	The method of claim 1, wherein the compound is a peptide.
1	21		The method of claim 20, wherein the peptide is circular.
1	22	2.	The method of claim 1, wherein the compound is an siRNA
2	molecule.		
1	23	3.	A method for identifying a compound that modulates cell cycle
2	arrest, the method	d con	aprising the steps of:
3	(i)	cont	acting a cell comprising a target polypeptide or fragment thereof or
4	inactive variant tl	hereo	f, selected from the group consisting of flap structure specific
5	endonuclease 1 (FEN	1), protein kinase C ζ (PKC- ζ), phospholipase C- β 1 (PLC- β 1),
6	protein tyrosine k	cinas	e 2 (FAK), protein tyrosine kinase 2b (FAK2), casein kinase 2
7	(CK2), cMET tyr	rosine	e kinase (cMET), REV1 dCMP transferase (REV1),
8	apurinic/apyrimic	dinic	nuclease 1 (APE1), cyclin dependent kinase 3 (CDK3), PIM1
9	kinase (PIM1), co	ell di	vision cycle 7 kinase (CDC7L1), cyclin dependent kinase 7
10	(CDK7), cytokin	e ind	ucible kinase (CNK), potentially prenylated protein tyrosine
11	phosphatase (PR)	L-3),	serine threonine kinase 2 (STK2) or (NEK4), cyclin dependent
12	serine threonine l	kinas	e (NKIAMRE), or histone acetylase (HBO1), or fragment thereof
13	with the compour	nd, th	ne target polypeptide encoded by the complement of a nucleic acid
14	that hybridizes un	nder	stringent conditions to a nucleic acid encoding a polypeptide having
15	an amino acid se	quen	ce selected from the group consisting of SEQ ID NO:14, 2, 4, 6, 8,
16	10, 12, 16, 18, 20), 22,	24, 26, 28, 30, 32, 34, and 36; and
17	(ii	i) det	ermining the physical effect of the compound upon the target
18	polypeptide or fr	agme	ent thereof or inactive variant thereof; and
19	(ii	ii) de	termining the chemical or phenotypic effect of the compound upon
20	a cell comprising	g the	target polypeptide or or fragment thereof or inactive variant thereof,
21	thereby identifying	ng a	compound that modulates cell cycle arrest.
1	24	4.	A method of modulating cell cycle arrest in a subject, the method
2	comprising the s	tep o	f administering to the subject a therapeutically effective amount of a

25. The method of claim 24, wherein the subject is a human.

compound identified using the method of claim 1.

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- 1 26. The method of claim 25, wherein the subject has cancer.
- 1 27. The method of claim 24, wherein the compound is a small organic
- 2 molecule.
- 1 28. The method of claim 24, wherein the compound is an antisense
- 2 molecule.
- 1 29. The method of claim 24, wherein the compound is an antibody.
- 1 30. The method of claim 24, wherein the compound is a peptide.
- 1 31. The method of claim 30, wherein the peptide is circular.
- 1 32. The method of claim 24, wherein the compound is an siRNA
- 2 molecule.
- 1 33. The method of claim 24, wherein the compound inhibits cancer cell
- 2 proliferation.
- 1 34. A method of modulating cell cycle arrests in a subject, the method
- 2 comprising the step of administering to the subject a therapeutically effective amount of a
- 3 target polypeptide or fragment thereof or inactive variant thereof, selected from the group
- 4 consisting of flap structure specific endonuclease 1 (FEN1), protein kinase C ζ (PKC-ζ),
- 5 phospholipase C- β 1 (PLC- β 1), protein tyrosine kinase 2 (FAK), protein tyrosine kinase
- 6 2b (FAK2), casein kinase 2 (CK2), cMET tyrosine kinase (cMET), REV1 dCMP
- 7 transferase (REV1), apurinic/apyrimidinic nuclease 1 (APE1), cyclin dependent kinase 3
- 8 (CDK3), PIM1 kinase (PIM1), cell division cycle 7 kinase (CDC7L1), cyclin dependent
- 9 kinase 7 (CDK7), cytokine inducible kinase (CNK), potentially prenylated protein
- tyrosine phosphatase (PRL-3), serine threonine kinase 2 (STK2) or (NEK4), cyclin
- dependent serine threonine kinase (NKIAMRE), or histone acetylase (HBO1), or
- fragment thereof with the compound, the target polypeptide encoded by the complement
- of a nucleic acid that hybridizes under stringent conditions to a nucleic acid encoding a
- polypeptide having an amino acid sequence selected from the group consisting of SEQ ID
- NO:14, 2, 4, 6, 8, 10, 12, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, and 36.

1	35. A method of modulating cell cycle arrest in a subject, the method
2	comprising the step of administering to the subject a therapeutically effective amount of a
3	nucleic acid encoding a target polypeptide or fragment thereof or inactive variant thereof,
4	selected from the group consisting of flap structure specific endonuclease 1 (FEN1), protein
5	kinase C ζ (PKC-ζ), phospholipase C-β1 (PLC-β1), protein tyrosine kinase 2 (FAK), protein
6	tyrosine kinase 2b (FAK2), casein kinase 2 (CK2), cMET tyrosine kinase (cMET), REV1
7	dCMP transferase (REV1), apurinic/apyrimidinic nuclease 1 (APE1), cyclin dependent
8	kinase 3 (CDK3), PIM1 kinase (PIM1), cell division cycle 7 kinase (CDC7L1), cyclin
9	dependent kinase 7 (CDK7), cytokine inducible kinase (CNK), potentially prenylated protein
10	tyrosine phosphatase (PRL-3), serine threonine kinase 2 (STK2) or (NEK4), cyclin dependent
11	serine threonine kinase (NKIAMRE), or histone acetylase (HBO1), or fragment thereof with
12	the compound, the target polypeptide encoded by the complement of a nucleic acid that
13	hybridizes under stringent conditions to a nucleic acid encoding a polypeptide having an
14	amino acid sequence selected from the group consisting of SEQ ID NO:14, 2, 4, 6, 8, 10, 12,
15	16, 18, 20, 22, 24, 26, 28, 30, 32, 34, and 36.
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1	36. A CK2-specific siRNA molecule comprising the sequence
2	AACATTGAATTAGATCCACGT, wherein the siRNA molecule is from 21 to 30 nucleotide

1 37. The CK2-specific siRNA molecule of claim 36 consisting of the sequence AACATTGAATTAGATCCACGT and its complement as active portion.

base pairs in length.

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- 1 38. A method of inhibiting expression of a CK2 gene in a cell, the method 2 comprising contacting the cell with a CK2-specific siRNA molecule comprising the sequence 3 AACATTGAATTAGATCCACGT, wherein the siRNA molecule is from 21 to 30 nucleotide 4 base pairs in length.
- 1 39. A PIM1-specific siRNA molecule comprising the sequence 2 AAAACTCCGAGTGAACTGGTC, wherein the siRNA molecule is from 21 to 30 3 nucleotide base pairs in length.
- 1 40. The PIM1-specific siRNA molecule of claim 39 consisting of the 2 sequence AAAACTCCGAGTGAACTGGTC and its complement as active portion.

1	41. A method of inhibiting expression of a PIM1 gene in a cell, the method
2	comprising contacting the cell with a PIM1-specific siRNA molecule comprising the
3	sequence AAAACTCCGAGTGAACTGGTC, wherein the siRNA molecule is from 21 to 30
4	nucleotide base pairs in length.
1	42. An Hbo1-specific siRNA molecule comprising the sequence
2	AACTGAGCAAGTGGTTGATTT, wherein the siRNA molecule is from 21 to 30 nucleotide
3	base pairs in length.
1	43. The Hbo1-specific siRNA molecule of claim 42 consisting of the
2	sequence AACTGAGCAAGTGGTTGATTT and its complement as active portion.
1	44. A method of inhibiting expression of an Hbol gene in a cell, the
2	method comprising contacting the cell with an Hbo1-specific siRNA molecule comprising
3	the sequence AACTGAGCAAGTGGTTGATTT, wherein the siRNA molecule is from 21 to
4	30 nucleotide base pairs in length.